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HUMAN TELOMERASE

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG      60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu      20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG     120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln      40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG     180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp      60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG     240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu      80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC     300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly     100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC     360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg     120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG     420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu     140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG     480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal     160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT     540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla     180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA     600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu     200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT     660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly     220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT     720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg     240
```

Fig. 1A

```
GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC   780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly   260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA   840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu   280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC   900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly   300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT   960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro   320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG  1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln   340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC  1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu   360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC  1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro   380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC  1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis   400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC  1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr   420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG  1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu   440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG  1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln   460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC  1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer   480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT  1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis   500
```

Fig. 1B

```
GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG   1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu    520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC   1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle    540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC   1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe    560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC   1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal    580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG   1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu    600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA   1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg    620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG   1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal    640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA   1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla    660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG   2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal    680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG   2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln    700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC   2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle    720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC   2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys    740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG   2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys    760
```

Fig. 1C

```
AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG   2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu    780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG   2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu    800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC   2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle    820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG   2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu    840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC   2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp    860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG   2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla    880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG   2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu    900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT   2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal    920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG   2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu    940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC   2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe    960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG   2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu    980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC   3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn   1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA   3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro   1020
```

Fig. 1D

```
TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC  3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls  1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC  3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly  1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC  3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu  1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG  3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln  1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC  3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn  1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACtgatggccacccgcccacagccag  3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp                          1132

Gccgagagcagacaccagcagccctgtcacgccgggctctacgtcccagggagggagggg  3480
Cggcccacacccaggcccgcaccgctgggagtctgaggcctgagtgagtgtttggccgag  3540
gcctgcatgtccggctgaaggctgagtgtccggctgaggcctgagcgagtgtccagccaa  3600
gggctgagtgtccagcacacctgccgtcttcacttccccacaggctggcgctcggctcca  3660
ccccagggccagcttttcctcaccaggagcccggcttccactccccacataggaatagtc  3720
catccccagattcgccattgttcacccctcgccctgccctcctttgccttccacccccac  3780
catccaggtggagaccctgagaaggaccctgggagctctgggaatttggagtgaccaaag  3840
gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgggtcaaatt  3900
ggggggaggtgctgtgggagtaaaatactgaatatatgagtttttcagttttgaaaaaaa  3960
aaaa                                                          3964
```

Fig. 1E

```
Euplotes    1 ----------------------MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCR--NQSQSHYKDLEDIK
HT1         1 RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDAR-PPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGA
EST2        1 ----------------------------------------------MKILFEFIQDKLDID--LQTNSTYKENLKCG

Euplotes   56 IFAQTNIVATPRDYNEEDFKVIARK---------EVFSTGLMIELIDKCLVELLSSSDVSDRQKLQCFGFQLKGNQ-LAK
HT1        80 RGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAY---QVCGPPLYQLGAATQA
EST2       30 HFNGLDEILTT-CFALPNSRKIALP---------CLPGDLSHKAVIDHCIIYLLTGELYNN---VLTFGYKIARNEDVNK

Euplotes  126 THLLTALSTQKQYFFQDEWNQVRAMIGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGAADMNE
HT1       157 RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG
EST2       97 SLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQ-FFTQIVGNRCNEPHLPPKWVQRSSSS-------

Euplotes  206 PRCCSTCKYNVKNEKDHFLNNI----------------------------NVPNWNNMKSRTRIFYCTHFNRNNQFF
HT1       237 PSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDK--EQLR
EST2      169 ----SATAAQIKQLTEPVTN----------------------------------------KQFLHKLNIN-SSSFF

Euplotes  255 KKHEFVSNKNNISAM-DRAQTIFTNI--------FRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRE
HT1       315 PSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRY-WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTP
EST2      200 PYSKILPSSSSIKKLTDLREAIFP----------TNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPLEGT--

                                                                    Telomerase domain
Euplotes  326 RK-----QKIENLINKTREEKS--KYYEELFSYTTDNKCVTQFINEFFYNILPKDFLTGR-NRKNFQKKVKKYVELNKHE
HT1       394 AAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHA
EST2      268 ---------VLDLSHLSRQ--------------SPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNG

Euplotes  398 LIHKNLLLEKINTREISWMQVET-SAKHFYYFDHENIYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW
HT1       474 KLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVW
EST2      324 YLPFDSLLKKLRLKDFRWLFISD-IWFTKHNFENLN-QLAICFISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTW

                                                                  Motif 1  Motif2
Euplotes  477 DVIMKMSIADLKK-ETLAEVQEKEVEEWKKSL-GFAPGKLRLIPKKTT--FRPIMTFNKKIVNSDRK--TTKLTTNTKLL
HT1       554 SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG--LRPIVNMDYVVGARTFRREKRAERLTSRVK
EST2      401 NKLITPFIVEYFK-TYLVENNVCRNHNSYTLS-NFNHSKMRIIPKKSNNEFRIIAIPCRGADEEEFT--IYKENHKNAIQ
```

Fig. 2A

```
                                                                                 Motif A
Euplotes  551 NSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQP-KLFFATMDIEKCYDSVNREKLSTFLKTTKLLSS
HT1       632 ALFSVLNYERARR--PGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQN
EST2      477 PTQKILEYLRNKRPTSFTKIYSPTQIADRIKEFKQRLLKKFNNVLP-ELYFMKFDVKSCYDSIPRMECMRILKDALKNEN

Euplotes  629 DFWIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVEAK-CRNYFKKD
HT1       710 TYCVRRYAVVQKAAHGHVRKAFKSHVS-------------TLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSG
EST2      556 GFFVRSQYFFN-TNTGVLKLFNVVN---------------A--SRVPKPYELYIDNVRTVHLSNQDVINVV-EMEIFKT-

                                    Motif B                                Motif C
Euplotes  708 NLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
HT1       777 LFDVFLRFMCHHAVRIR-GKSYVQCQGIPQGSILSTLLCSLCYGDMEN---KLFAGIRRD------GLLLRLVDDFLLVT
EST2      616 --ALWVEDKCYIR-----------EDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQD------TLILKLADDFLIIS

                               Motif D                          Motif E
Euplotes  788 TQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMKTLALMPNINLRI
HT1       847 PHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGG-TAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYAR--
EST2      677 TDQQ-QVINIKKLAMG----GFQKYNAKANRDKILAVS--------SQSDDDTVIQFCAMHIFVKELEVWKHSSTMN---

Euplotes  868 EGILCTLNLNMQTKKASMWLKKKLKSFLMNNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEY--KDHFKKNLAM
HT1       924 TSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTF
EST2      741 -------NFHIRSKSS----KGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSA--FKDLSINVTQ

Euplotes  946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIEIFSTKKYIFNRVCMILKAKEAKLKSDQCQS
HT1      1004 FLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC-HQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGT
EST2      808 NMQFHSFLQRIIEMTVSG----CPITKCDPLIEYEVR--FTI--LNGFLESLSSNTSKF-KDNIILLRKEIQHLQAYIYI

Euplotes 1026 LIQYDA----------------
HT1      1083 TLTALEAAANPALPSDFKTILD
EST2      879 YIHIVN----------------
```

Fig. 2B

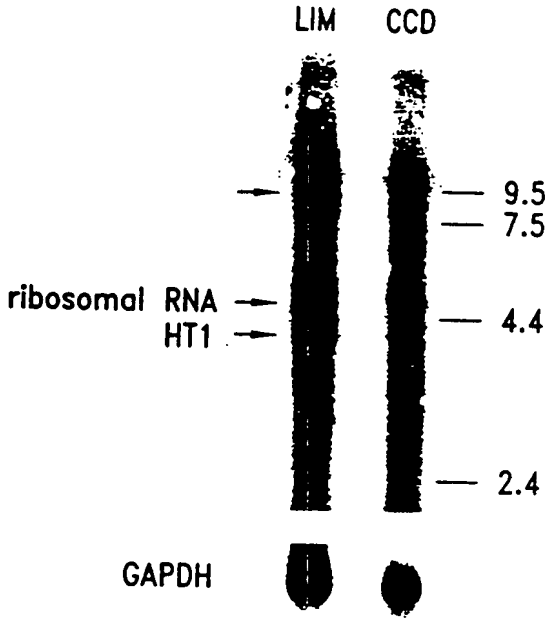

Fig. 3

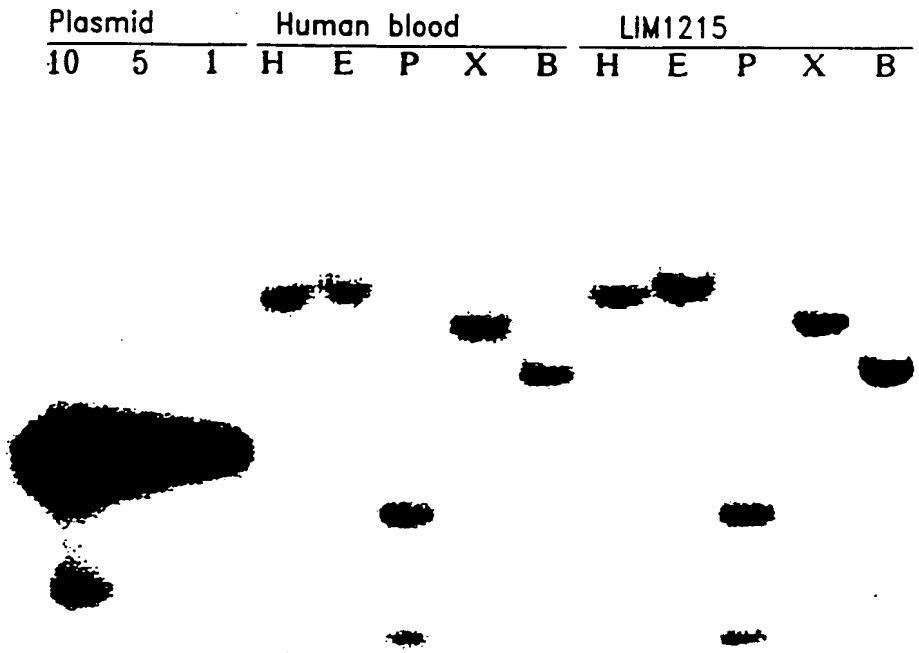

Fig. 4

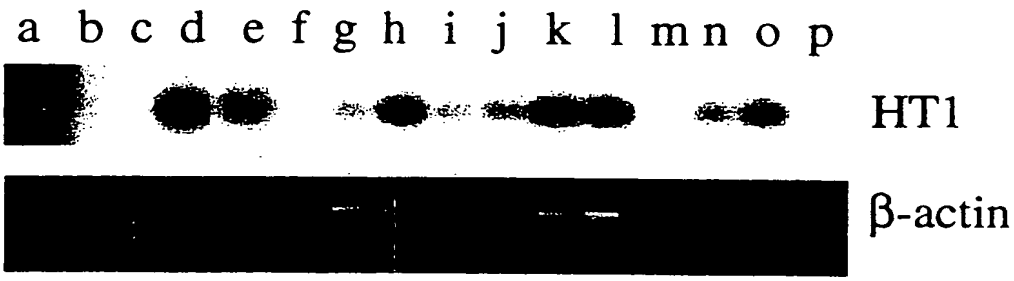

Fig. 5

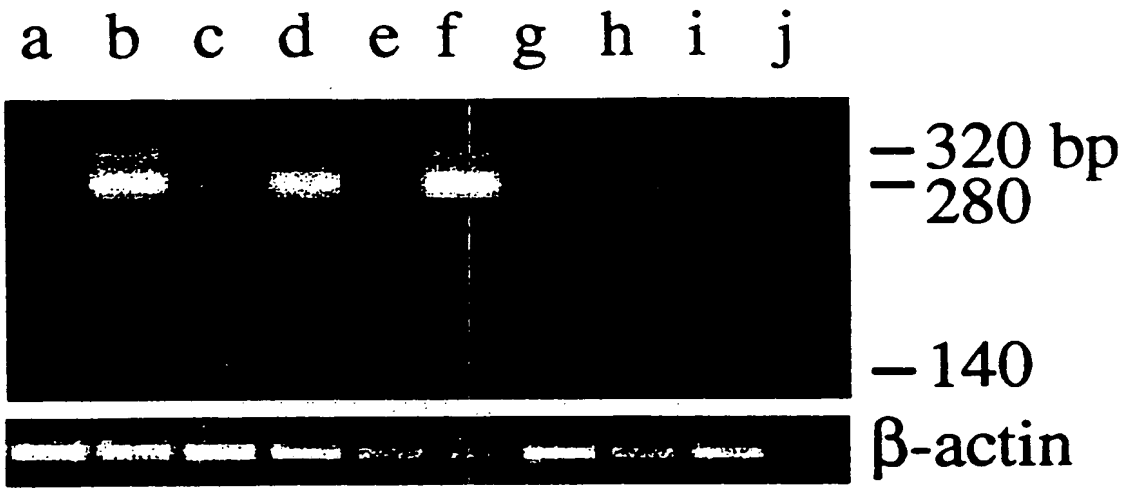

Fig. 6

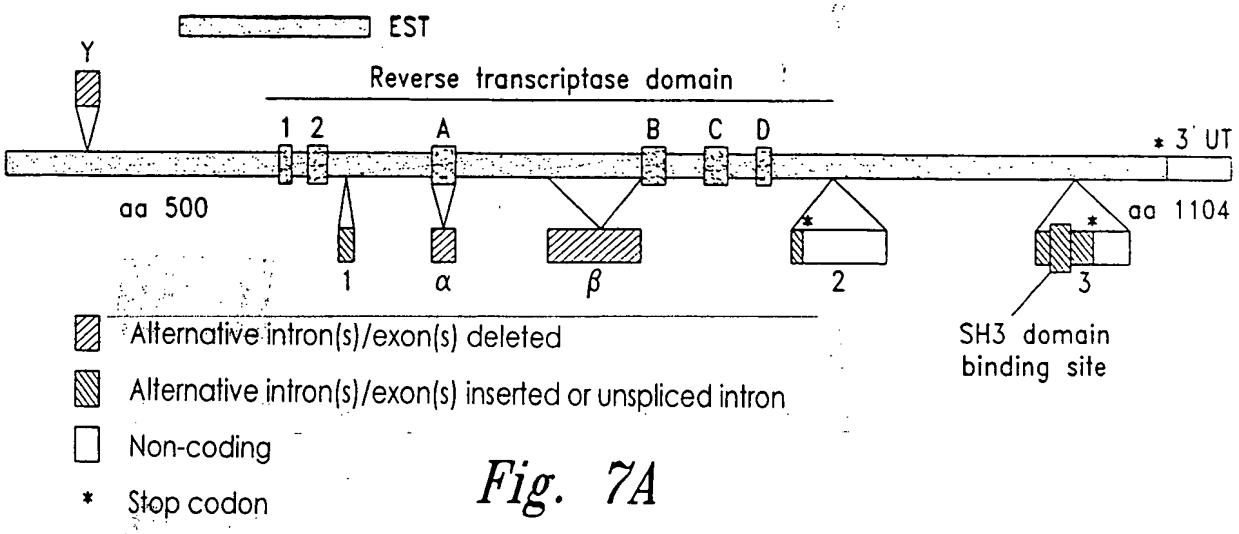

Fig. 7A

Variants:	1	α	β	2	3
RT-PCR product	NO	+	+	NO	+ & −
PCR from LIM1215 lib.	−	+	−	+	NO
RT-PCR product	NO	−	+	NO	+
53.2 cDNA	−	−	−	−	NO

Fig. 7B

```
                222                                                  223
Y   5'-CCAGGTG|ggcctc                                    gcaggtg|TCCTGCC-3'

                1950                                                 1952
1   5'-AAAGAGG|GTGGCTG.....................................AACAGAA|GCCGAGC-3'

                2130                                                 2167
a   5'-TGTCAAG|gtggatg.....................................cccccag|GACAGGC-3'

                2286                                                 2468
b   5'-GAGCCAC|gtctcta.....................................ggggcaa|GTCCTAC-3'

                2843                                                 2844
2   5'-ACTCCAG|GTGAGCG.....................................XXXXXXX|CTATGCC-3'

                3157
3   5'-AACGCAG|CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAGATGG
      T  A  A  E  E  N  I  L  V  V  T  P  A  V  L  G  S  G  Q  P  E  M  E

          AGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTG
            P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G

                                                        3158
          GGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG|GGATGTC-3'
            L  G  L  *
```

Fig. 7C

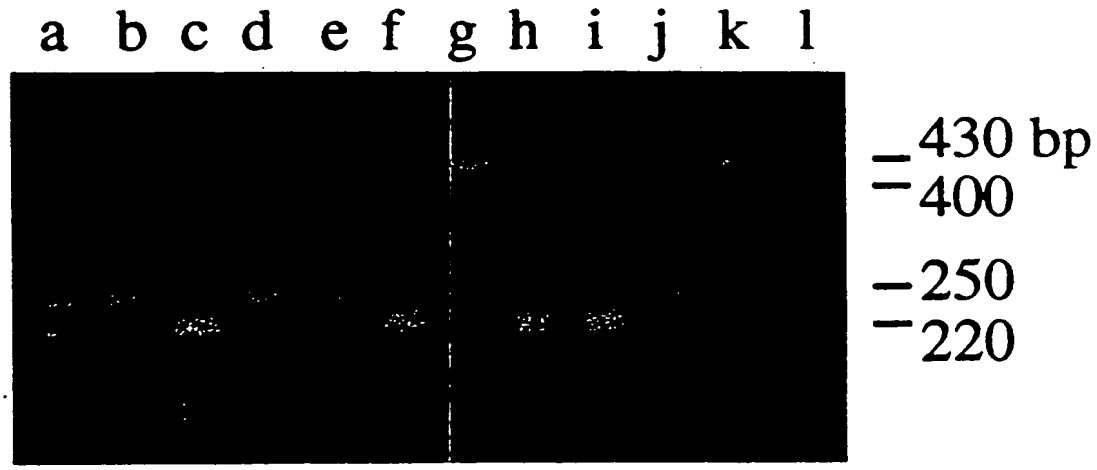

Fig. 8

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCAC
 K  A  A  H  G  H  V  R  K  A  F  K  S  H

                                                                                                                GTCCTACGTCCAGTG
                                                                                                                 V  L  R  P  V

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P  V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P  A  F  G  G

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 *
```

Fig. 11AA

Reference protein (ver. 2)

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG      60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu      20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG     120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln      40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG     180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp      60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTG
AspAlaArgProProProAlaAlaProSerPheArgGlnVal

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAG
G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E
 A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R
  P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E

AGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
S  S  A  G  D  S  G  R  F  P  R  R
 A  A  Q  A  T  Q  G  A  S  P  A  G
  Q  R  R  R  L  R  A  L  P  P  Q  V


TCCTGCCTGAAGGAGCTG     240
SerCysLeuLysGluLeu      80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC     300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly     100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC     360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg     120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG     420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu     140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG     480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal     160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT     540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla     180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA     600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu     200
```

Fig. 11AB

```
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT   660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly   220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT   720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg   240

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC   780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly   260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA   840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu   280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC   900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly   300

CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT   960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro   320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG  1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln   340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC  1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu   360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC  1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro   380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC  1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis   400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC  1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr   420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG  1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu   440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG  1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln   460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC  1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer   480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT  1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis   500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG  1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu   520
```

Fig. 11AC

```
CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC  1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle   540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC  1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe   560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC  1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal   580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG  1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu   600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA  1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg   620

CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG  1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal   640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA  1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla   660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG  2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal   680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG  2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln   700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC  2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle   720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC  2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys   740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG  2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys   760

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG  2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu   780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG  2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu   800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC  2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle   820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG  2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu   840
```

Fig. 11AD

```
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC  2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp   860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG  2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla   880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG  2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu   900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT  2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal   920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG  2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu   940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC  2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe   960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG  2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu   980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC  3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn  1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA  3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro  1020

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC  3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls  1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC  3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly  1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC  3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu  1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG  3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln  1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC  3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn  1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC                          3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp                          1132
```

Fig. 11AE

Truncated protein 3 (ver. 2)

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

                                                GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                                                G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
                                                A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
                                                P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11AF

```
                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  R

                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
 *

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA....
```

Fig. 11AG

Altered C-terminus protein (ver. 2)

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
 A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
  P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11AH

```
                                                                                                                    .
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L
                                                                                                                    .
GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
                                                                                                                    .
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D
                                                                                                                    .
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E
                                                                                                                    .
GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F
                                                                                                                    .
TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q
                                                                                                                    .
GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D
                                                                                                                    .
TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C
                                                                                                                    .
CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D
                                                                                                                    .
TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P
                                                                                                                    .
TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  S
                                                                                                                    .
CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
 Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F  K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S  L  F  L  D
                                                                                                                    .
TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
 L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  V  W  K  N
                                                                                                                    .
CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
 P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A  E
                                                                                |
                                                                                CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
                                                                                 E  E  N  I  L  V  V  T  P  A  V  L  G  S
                                                                                                                    .
GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
 G  Q  P  E  M  E  P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G  L  G  L  *
```

Fig. 11AI

Protein that lacks motif A (ver. 2)

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

                                                GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                                                G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
                                                 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
                                                  P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
                                                 |.
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L
```

Fig. 11AJ

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG                                    GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K                                        D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D
```

Fig. 11AK

CTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCT

GAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCAC

CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAA

GGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAA

AATACTGAATATATGAGTTTTTCAGTTTTGA

Fig. 11AL

Truncated protein that lacks motif A (ver. 2)

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

                                                                .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
                                                                CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
                                                                R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

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                                                                      GGCCTCCCCGGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                                                                      G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
                                                                      A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
                                                                       P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
                                                                      |.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

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CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

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GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

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ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

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CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

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ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

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AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L
```

Fig. 11AM

```
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAG                                GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K                                  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
 *

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA....
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Fig. 11AN

Lacks motif A and altered C-terminus (ver. 2)

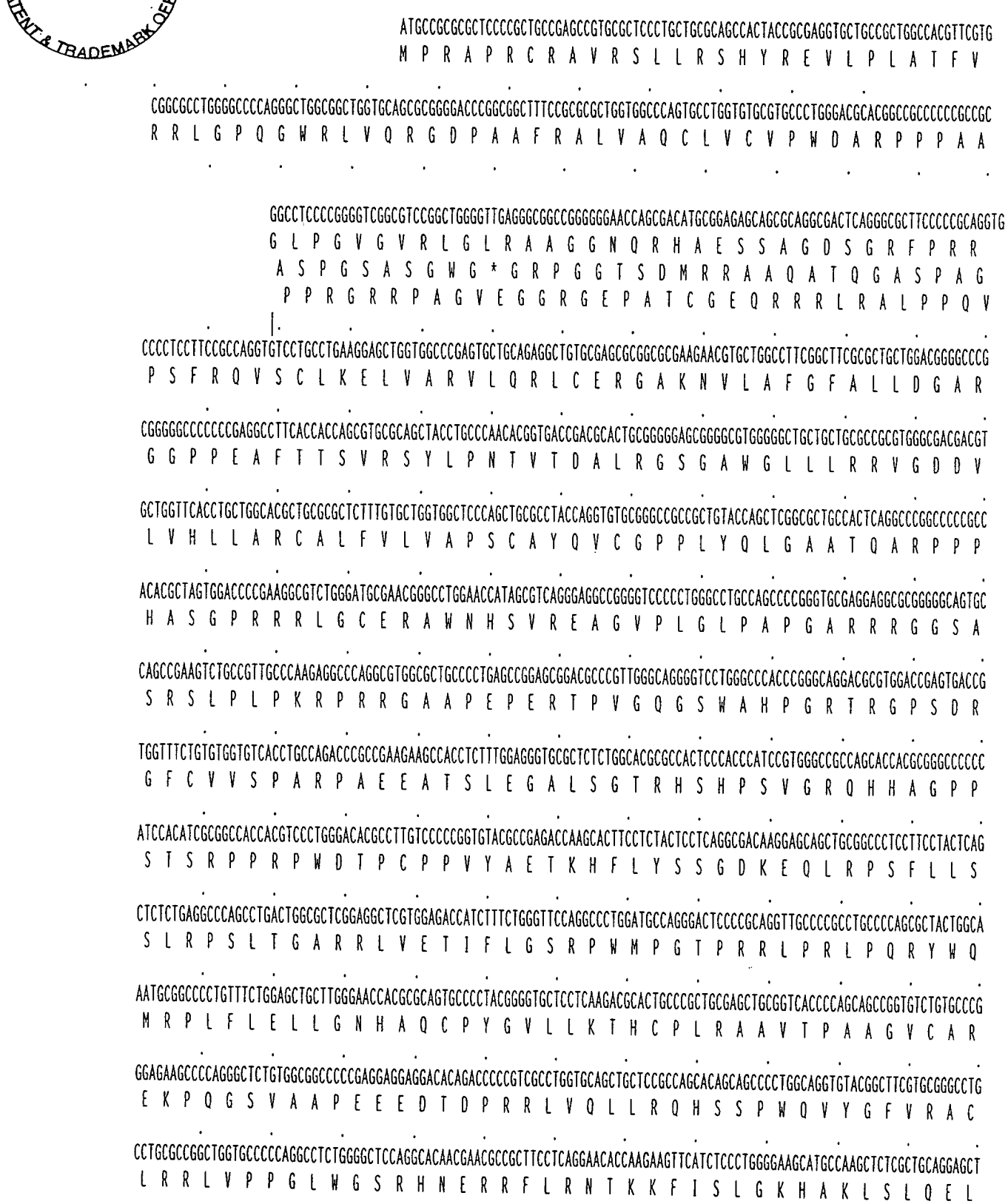

Fig. 11AO

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GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAG                                GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K                                  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
 Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F  K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S  L  F  L  D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
 L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  V  W  K  N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
 P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A  E
                                                                          |
                                                                         CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
                                                                          E  E  N  I  L  V  V  T  P  A  V  L  G  S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
 G  Q  P  E  M  E  P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G  L  G  L  *
```

Fig. 11AP

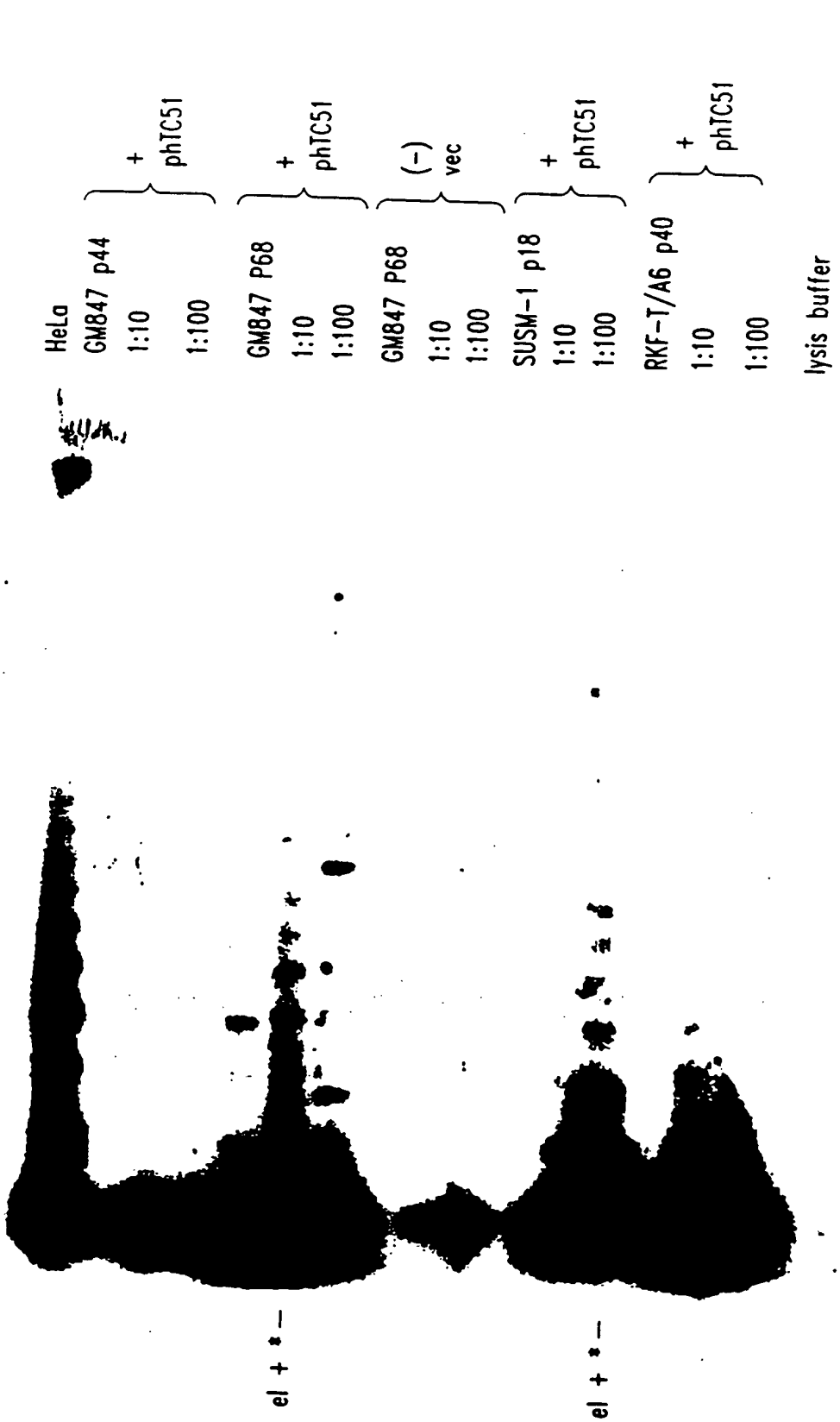

Fig. 12

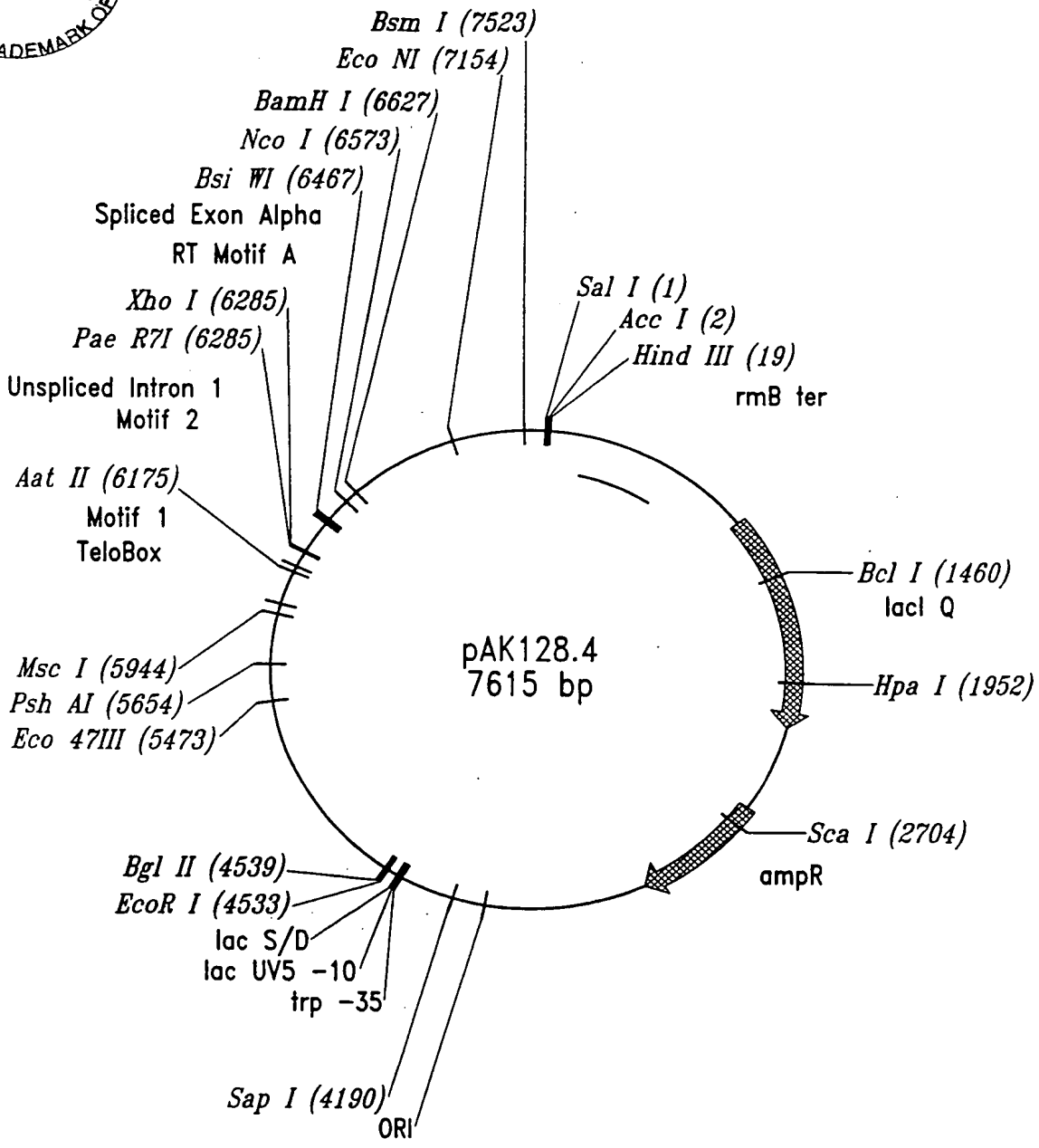

Fig. 13A

LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out

```
   1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt
 121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
 181 tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
 241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
 361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
 421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
 481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
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 901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
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1021 ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat
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1141 cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
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1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
1621 cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc
1681 tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac
1741 gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc
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2041 atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg
2281 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt
2461 gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag
2581 aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta
2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
```

Fig. 13B

```
2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag
2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg
2941 tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc
3001 ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg
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Fig. 13C

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Fig. 13D

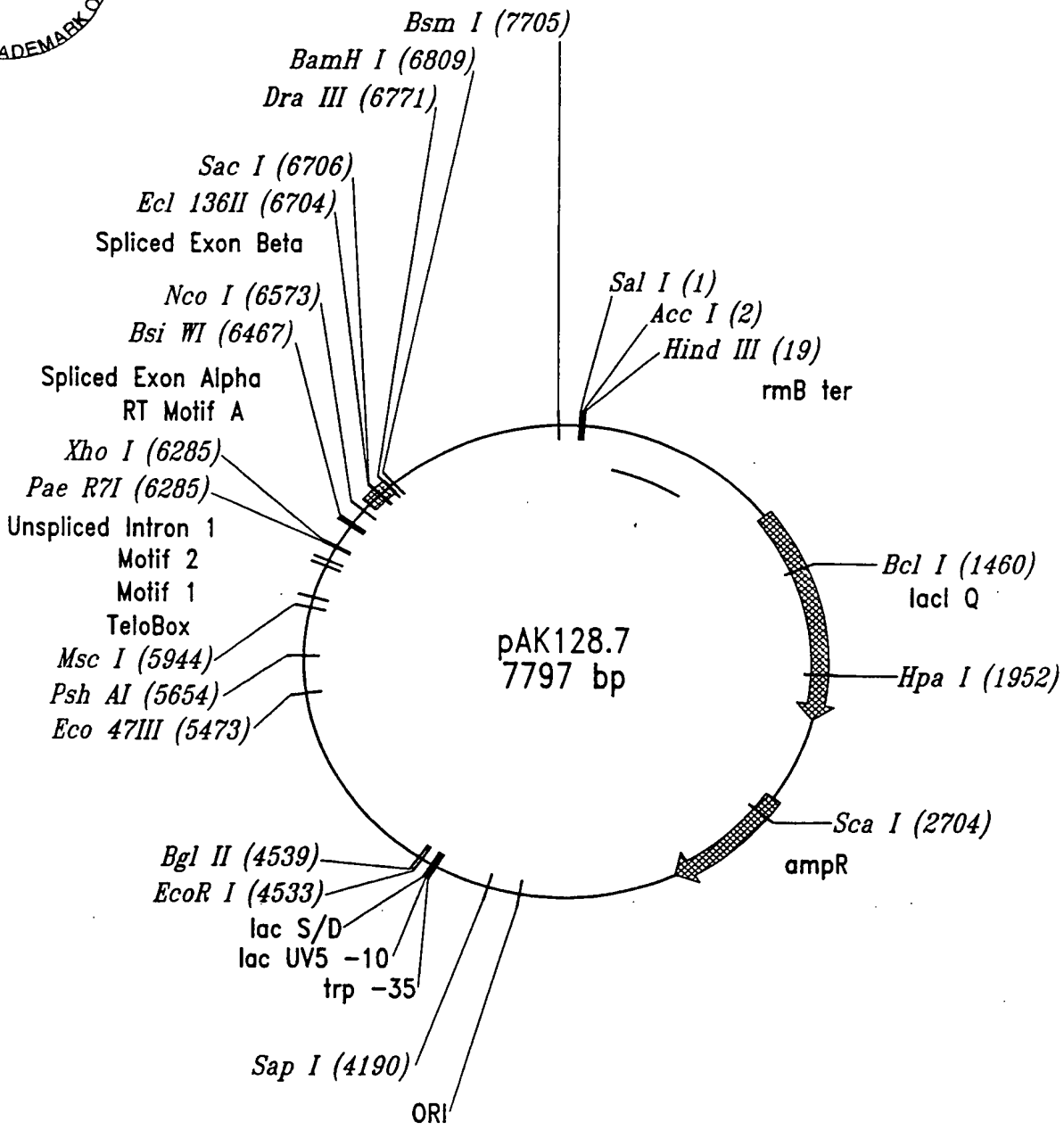

Fig. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

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  61 aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt
 121 aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
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 241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
 301 aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc
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 541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa
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```

Fig. 14B

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Fig. 14C

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Fig. 14D

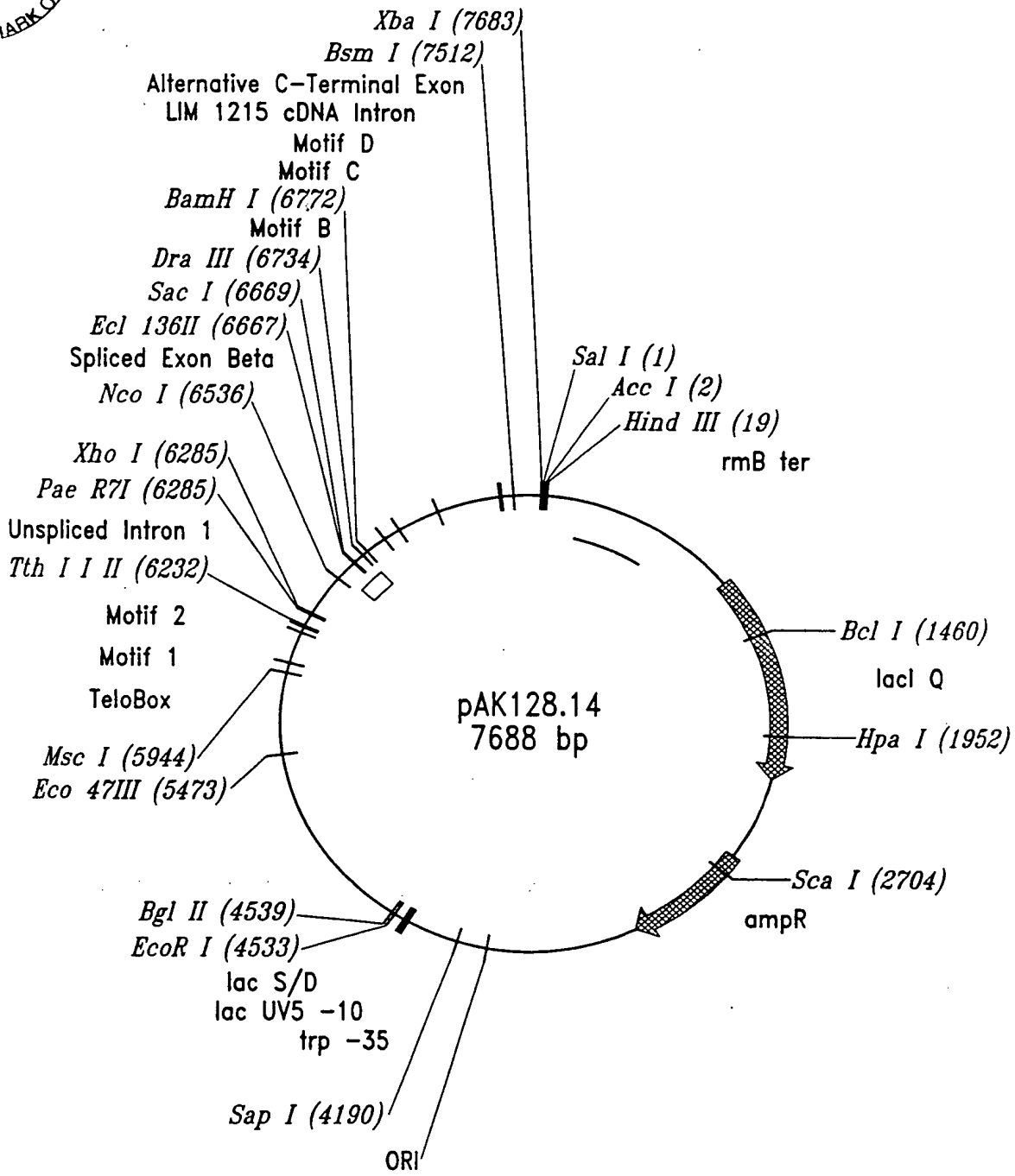

Fig. 15A

LOCUS pAKI28.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

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 361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
 421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
 481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
 541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa
 601 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac
 661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
 721 gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg
 781 ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt
 841 gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc
 901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
 961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat
1081 tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg
1441 cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg
1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
1621 cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc
1681 tgcgtctggc tggctggcat aaatatctca ctcgcaatca attcagccg atagcggaac
1741 gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc
1981 tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca
2041 atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg
2281 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt
2461 gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag
2581 aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta
2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
```

Fig. 15B

```
2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag
2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg
2941 tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc
3001 ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg
3061 cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga
3181 cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac
3241 tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca
3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac
3481 cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa
3541 ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc
3601 accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc ctgttaccag
3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac
3721 cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc
3781 gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc
3841 ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca
3901 cgagggagct tccagggggа aacgcctggt atctttatag tcctgtcggg tttcgccacc
3961 tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg
4021 ccagcaacgc ggccttttta cggttcctgg ccttttgctg gccttttgct cacatgttct
4081 ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata
4141 ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc
4201 gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt
4261 ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag
4321 ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc
4381 aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa
4441 tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag
4501 cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
4561 tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct
4621 tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca
4681 gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc
4741 tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc
4801 tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg
4861 ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac
4921 gggcctggaa ccatagcgtc agggaggccg gggtcccccт gggcctgcca gccccgggtg
4981 cgaggaggcg cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg
5041 gcgctgcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca
5101 ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag
5161 aagccacctc tttggagggt gcgctctctg gcacgcgcca ctcccaccca tccgtgggcc
5221 gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt
5281 gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc
5341 tgcggccctc cttcctactc agctctctga ggcccagcct gactggcgct cggaggctcg
5401 tggagaccat ctttctgggt tccaggccct ggatgccagg gactccccgc aggttgcccc
5461 gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg
5521 cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc
```

Fig. 15C

```
5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg
5641 aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg
5701 tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca
5761 ggcacaacga acgccgcttc ctcaggaaca ccaagaagtt catctccctg gggaagcatg
5821 ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc
5881 gcaggagccc aggggttggc tgtgttccgg ccgcagagca ccgtctgcgt gaggagatcc
5941 tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct
6001 tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct
6061 ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc
6121 tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac
6181 tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg
6241 gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac
6301 tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc
6361 tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg
6421 acccgccgcc tgagctgtac tttgtcaagg acaggctcac ggaggtcatc gccagcatca
6481 tcaaacccag aacacgtact gcgtgcgtcg gtatgccgtg gtccagaagg ccgcccatgg
6541 gcacgtccgc aaggccttca agagccacgt ctctaccttg acagacctcc agccgtacat
6601 gcgacagttc gtggctcacc tgcaggagac cagcccgctg agggatgccg tcgtcatcga
6661 gcagagctcc tccctgaatg aggccagcag tggcctcttc gacgtcttcc tacgcttcat
6721 gtgccaccac gccgtgcgca tcaggggcaa gtcctacgtc cagtgccagg ggatcccgca
6781 gggctccatc ctctccacgc tgctctgcag cctgtgctac ggcgacatgg agaacaagct
6841 gtttgcgggg attcggcggg acgggctgct cctgcgtttg gtggatgatt tcttgttggt
6901 gacacctcac ctcacccacg cgaaaacctt cctcaggacc ctggtccgag gtgtccctga
6961 gtatggctgc gtggtgaact tgcggaagac agtggtgaac ttccctgtag aagacgaggc
7021 cctgggtggc acggcttttg ttcagatgcc ggcccacggc ctattccccc ggtgcggcct
7081 gctgctggat acccggaccc tggaggtgca gagcgactac tccagctatg cccggacctc
7141 catcagagcc agtctcacct tcaaccgcgg cttcaaggct gggaggaaca tgcgtcgcaa
7201 actctttggg gtcttgcggc tgaagtgtca cagcctgttt ctggatttgc aggtgaacag
7261 cctccagacg gtgtgcacca acatctacaa gatcctcctg ctgcaggcgt acaggtttca
7321 cgcatgtgtg ctgcagctcc catttcatca gcaagtttgg aagaacccca cattttcct
7381 gcgcgtcatc tctgacacgg cctccctctg ctactccatc ctgaaagcca agaacgcagg
7441 gatgtcgctg ggggccaagg gcgccgccgg ccctctgccc tccgaggccg tgcagtggct
7501 gtgccaccaa gcattcctgc tcaagctgac tcgacaccgt gtcacctacg tgccactcct
7561 ggggtcactc aggacagccc agacgcagct gagtcggaag ctcccgggga cgacgctgac
7621 tgccctggag gccgcagcca acccggcact gccctcagac ttcaagacca tcctggactg
7681 atctagag
```

Fig. 15D

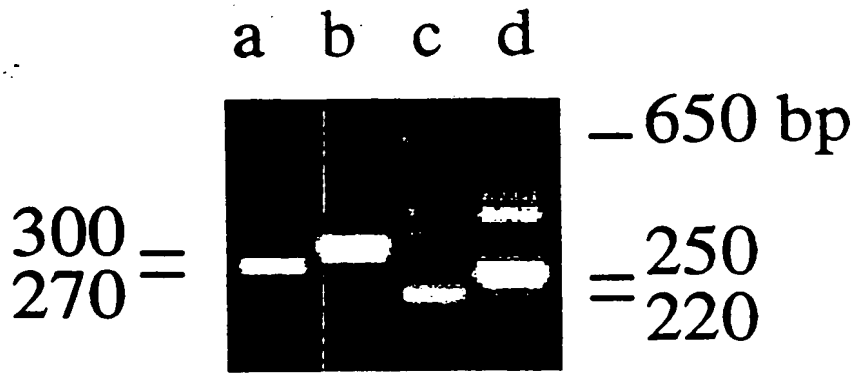

Fig. 9

sequence "Y" 104-105 bases
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases
GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases
GTGGATGTGACGGGCGCGTACGACACCATCCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases
GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys

partial sequence "2" unknown length
GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG
Ter

GGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT
CAGATGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTG
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

Fig. 10A

sequence "3" 159 bases
CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
GlyValGlyLeuGlyLeu *

sequence "X" unknown length
...GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGA
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGGCATGG
GTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCT
CACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTGG
CTGAGCAAGCCTCCTGAGGGGCTCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)
GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAAGTGCGTTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCACCCATTTGTGCGCACAGTGAGGTGGCCGAGGTGCCGGTGCCTCCA
GAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....

Fig. 10B

Truncated telomerase

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G

AAT--NNN--GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGACCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGG
```

Fig. 11A

CATGGGTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTCTATTG...

Fig. 11B

Truncated protein 1

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
 M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
 R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
 P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
 G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
 L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
 H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
 S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
 G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
 S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
 S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
 M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
 E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
 L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
```

Fig. 11C

```
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

                                                                                                GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
                                                                                                 V  A  V  L  W  F  T  F  L  F  N  Q  K

                                                                                                |
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  P  S  V  S  F  R  G  *
```

Fig. 11D

Truncated protein 2

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11E

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCAC
K A A H G H V R K A F K S H

GTCCTACGTCCAGTG
V L R P V

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
*

Fig. 11F

Reference protein

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG     60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu     20

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG    120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln     40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG    180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp     60

GACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG    240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu     80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC    300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly    100

TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGC    360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg    120

AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG    420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu    140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG    480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal    160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT    540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla    180

GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA    600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu    200

CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT    660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly    220

GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT    720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg    240

GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGC    780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly    260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA    840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu    280

GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC    900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly    300
```

Fig. 11G

```
CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT   960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro   320

TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG  1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln   340

CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC  1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu   360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC  1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro   380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC  1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis   400

GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC  1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr   420

CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG  1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu   440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG  1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln   460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC  1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer   480

AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT  1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis   500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG  1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu   520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC  1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle   540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC  1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe   560

TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC  1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal   580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG  1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu   600

CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA  1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg   620
```

Fig. 11H

```
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG  1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal   640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA  1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla   660

CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTG  2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal   680

CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG  2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln   700

GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC  2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle   720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC  2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys   740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG  2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys   760

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG  2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu   780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG  2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu   800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC  2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle   820

AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG  2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu   840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC  2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp   860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG  2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla   880

AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG  2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu   900

CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT  2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal   920

CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG  2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu   940
```

Fig. 11I

```
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC   2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe    960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG   2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu    980

AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC   3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn   1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA   3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro   1020

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC   3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls   1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC   3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly   1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC   3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu   1080

AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG   3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln   1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC   3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn   1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC                           3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp                           1132
```

Fig. 11J

Truncated protein 3

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11K

```
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
 *

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA....
```

Fig. 11L

Altered C-terminus protein

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
```

Fig. 11M

```
                                                                                                    .
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

                                                                                                    .
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

                                                                                                    .
GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

                                                                                                    .
TGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

                                                                                                    .
GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

                                                                                                    .
TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

                                                                                                    .
CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

                                                                                                    .
TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

                                                                                                    .
TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  S

                                                                                                    .
CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
 Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F  K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S  L  F  L  D

                                                                                                    .
TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
 L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  V  W  K  N

                                                                                                    .
CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
 P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A  E
                                                                                 |
                                                                                CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
                                                                                 E  E  N  I  L  V  V  T  P  A  V  L  G  S

                                                                                                    .
GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
 G  Q  P  E  M  E  P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G  L  G  L  *
```

Fig. 11N

Protein that lacks motif A

```
ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
 M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
 R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
 P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
 G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
 L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
 H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
 S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
 G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
 S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
 S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
 M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
 E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
 L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
```

Fig. 11O

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D

CTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCT

GAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCAC

CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAA

Fig. 11P

GGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAA

AATACTGAATATATGAGTTTTTCAGTTTTGA

Fig. 11Q

Truncated protein that lacks motif A

```
                                                                                                                    ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                                                                    M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
                                                                                                                    R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
                                                                                                                    P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
                                                                                                                    G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
                                                                                                                    L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
                                                                                                                    H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
                                                                                                                    S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
                                                                                                                    G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
                                                                                                                    S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
                                                                                                                    S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
                                                                                                                    M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
                                                                                                                    E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
                                                                                                                    L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
                                                                                                                    T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L
                                                                                                                    .     .     .     .     .     .     .     .     .     .     .     .     .     .     .
                                                                                                                    GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
                                                                                                                    M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
```

Fig. 11R

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA
*

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA.....

Fig. 11S

Lacks motif A and altered C-terminus

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11T

```
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  L  N  Y  E

GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTT
 R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P  E  L  Y  F

TGTCAAG                                     GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA
 V  K                                        D  R  L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y  A  V  V  Q

GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
 K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S  T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  E  T  S  P  L  R  D

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG
 A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G  L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S  Y  V  Q  C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA
 Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  R  L  V  D

TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCC
 D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  V  N  F  P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG
 V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  D  Y  S  S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA
 Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F  K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S  L  F  L  D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA
 L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I  L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  V  W  K  N

CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGA
 P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y  S  I  L  K  A  K  N  A  E
                                                                            |
                                                                           CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC
                                                                            E  E  N  I  L  V  V  T  P  A  V  L  G  S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
 G  Q  P  E  M  E  P  P  R  R  P  S  G  V  G  S  F  P  V  S  P  G  R  G  V  G  L  G  L  *
```

Fig. 11U

Truncated telomerase (ver. 2)

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

                                GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                                G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
                                 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
                                  P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
                                 |.
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L
```

Fig. 11V

GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AAT--NNN--GACAGTCACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGACCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGG

CATGGGTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTCTATTG...

Fig. 11W

Truncated protein 1 (ver. 2)

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M  P  R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  P  L  A  T  F  V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  D  P  A  A  F  R  A  L  V  A  Q  C  L  V  C  V  P  W  D  A  R  P  P  P  A  A

                                                GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                                                G  L  P  G  V  G  V  R  L  G  L  R  A  A  G  G  N  Q  R  H  A  E  S  S  A  G  D  S  G  R  F  P  R  R
                                                A  S  P  G  S  A  S  G  W  G  *  G  R  P  G  G  T  S  D  M  R  R  A  A  Q  A  T  Q  G  A  S  P  A  G
                                                P  P  R  G  R  R  P  A  G  V  E  G  G  R  G  E  P  A  T  C  G  E  Q  R  R  R  L  R  A  L  P  P  Q  V

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P  S  F  R  Q  V  S  C  L  K  E  L  V  A  R  V  L  Q  R  L  C  E  R  G  A  K  N  V  L  A  F  G  F  A  L  L  D  G  A  R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G  G  P  P  E  A  F  T  T  S  V  R  S  Y  L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  R  V  G  D  D  V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L  V  H  L  L  A  R  C  A  L  F  V  L  V  A  P  S  C  A  Y  Q  V  C  G  P  P  L  Y  Q  L  G  A  A  T  Q  A  R  P  P  P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H  A  S  G  P  R  R  R  L  G  C  E  R  A  W  N  H  S  V  R  E  A  G  V  P  L  G  L  P  A  P  G  A  R  R  R  G  G  S  A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  R  G  P  S  D  R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  H  A  G  P  P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S  T  S  R  P  P  R  P  W  D  T  P  C  P  P  V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  E  Q  L  R  P  S  F  L  L  S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S  L  R  P  S  L  T  G  A  R  R  L  V  E  T  I  F  L  G  S  R  P  W  M  P  G  T  P  R  R  L  P  R  L  P  Q  R  Y  W  Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  Y  G  V  L  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  V  C  A  R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E  K  P  Q  G  S  V  A  A  P  E  E  E  D  T  D  P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  V  R  A  C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S  L  Q  E  L
```

Fig. 11X

```
                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT
 T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F  L  H  W  L
                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
 M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  Q  S  I  G
                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
 I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  P  K  P  D


                                                                GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA
                                                                V  A  V  L  W  F  T  F  L  F  N  Q  K
                .   .   .   .   .   .   .   .   |   .   .   .   .   .   .   .
CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA
 G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  F  R  R  E  K  R  P  S  V  S  F  R  G  *
                .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
```

Fig. 11Y

Truncated protein 2 (ver. 2)

```
                                                                ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG
                                                                M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

                                                GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
                                                G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
                                                 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
                                                  P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
                                                  |
CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L
```

Fig. 11Z